SEQUENCE LISTING

<110>   University of Florida Research Foundation, Inc.
        Hannah, L. Curtis
        Lyerly Linebarger, Carla R.

<120>   Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130>   UF-371XC1 PCT

<150>   US 60/496,188
<151>   2003-08-18

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<170>   PatentIn version 3.2

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Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
            35                  40                  45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
        50                  55                  60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65                  70                  75                  80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85                  90                  95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100                 105                 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
            115                 120                 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
        130                 135                 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145                 150                 155                 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
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Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
            180                 185                 190
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Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
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Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
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Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
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Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                245             250                     255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln·Leu Leu Arg Glu Gln Phe
                260             265             270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
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Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
        290             295             300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305             310             315             320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
                325             330             335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
                340             345             350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
                355             360             365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
        370             375             380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385             390             395                     400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
                405             410             415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
                420             425             430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
        435             440             445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
            35                  40                  45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
        50                  55                  60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65              70                  75                      80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85                  90                  95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100                 105                 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
            115                 120                 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
        130                 135                 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145                 150                 155                 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
            165                 170                 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
            180                 185                 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
            195                 200                 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
        210                 215                 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225                 230                 235                 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
            245                 250                 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
            260                 265                 270
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Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
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Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305             310             315             320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
                325             330             335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
        340             345             350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
        355             360             365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
        370             375             380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385             390             395             400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
            405             410             415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
        420             425             430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
        435             440             445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
    450             455             460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465             470             475
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cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt     240

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                20   25   30

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
            35   40   45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys

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        50                      55                      60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65              70              75                      80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                85              90                      95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
            100             105             110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
        115             120             125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
    130             135             140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145             150             155             160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
            165             170             175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
            180             185             190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
        195             200             205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
    210             215             220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225             230             235             240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
            245             250             255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
            260             265             270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
            275             280             285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
    290             295             300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305             310             315             320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
            325             330             335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
            340             345             350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
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           355                    360                    365
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    370                375                380
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385                390                395                400
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Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
              405                410                415
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Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
              420                425                430
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Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
              435                440                445
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Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val
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Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465                470                475
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cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt     240

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Gln Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
        35                  40                  45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
    50                  55                  60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65                  70                  75                  80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                85                  90                  95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
            100                 105                 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
        115                 120                 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
    130                 135                 140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
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145   150   155   160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
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Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
                180   185   190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
                195   200   205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
     210   215   220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225   230   235   240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
                245   250   255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
                260   265   270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
          275   280   285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
     290   295   300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305   310   315   320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
                325   330   335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
                340   345   350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
          355   360   365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
     370   375   380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385   390   395   400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
                405   410   415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
                420   425   430

Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
          435   440   445

Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val

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        450                    455                    460

  Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
  465                    470                    475


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cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt     240

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tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac     420

tggtttcagg gtactgcaga tgctgtaagg cagtacttgt ggttgtttga ggagcataat     480

gtgatggaat ttctaattct tgctggcgat cacctgtacc ggatggacta tgaaaagttc     540

attcaggcac acagagaaac aaatgctgat attaccgttg ctgccctacc gatggatgag     600

aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aagggaggat cattgagttt     660

gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc     720

cttgatgacg tgagggcaaa ggaaatgcct tatattgcta gcatgggtat ctatgttttc     780

agcaaagatg taatgcttca gctcctccgt gaacaatttc ctgaagccaa tgactttgga     840

agtgaggtta ttccaggtgc aaccagcatt ggaaagaggg ttcaggctta tctgtatgat     900

ggttactggg aagatatcgg taccattgcg gcattttata atgcaaactt gggaataacc     960

aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct    1020

cgacacctgc caccttcaaa ggttcttgat gctgatgtga cagacagtgt tattggtgaa    1080

ggatgtgtta ttaaaaactg caagataaac cattctgtag ttggactccg atcttgcata    1140

tctgaaggtg ctatcataga ggacagttta ctaatgggtg cggactacta tgagacagaa    1200

gctgataaaa aactccttgc cgaaaaaggt ggcattccta ttggtattgg gaaaaattca    1260

tgcatcagga gagcaatcat tgacaagaat gctcgaattg gagacaatgt taagatactc    1320

aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaaggtgga    1380
```

attgtcacag tgatcaagga tgctttactc cctagtggaa cagttata   1428

<210> 10
<211> 476
<212> PRT
<213> zea mays

<400> 10

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
1   5   10   15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20   25   30

Asp Ser Glu Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
            35   40   45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
    50   55   60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65   70   75   80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
            85   90   95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
            100   105   110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
        115   120   125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
    130   135   140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145   150   155   160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
            165   170   175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
        180   185   190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
        195   200   205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
    210   215   220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225   230   235   240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly

```
                 245                    250                    255

    Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
            260                    265                    270

    Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
            275                    280                    285

    Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
            290                    295                    300

    Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
    305                    310                    315                    320

    Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
                325                    330                    335

    Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
                340                    345                    350

    Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
                355                    360                    365

    Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
            370                    375                    380

    Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
    385                    390                    395                    400

    Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
                405                    410                    415

    Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
                420                    425                    430

    Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
                435                    440                    445

    Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val
        450                    455                    460

    Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
    465                    470                    475
```

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<210> 11
<211> 1582
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form

<220>
<221> variation
```

<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 11
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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac  51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1           5                   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta  99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15               20              25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt  147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
             35              40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct  195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50              55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat  243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
             65              70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga  291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80              85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct  339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95              100             105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc  387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                 115             120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act  435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

             130             135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac  483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
             145             150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa  531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
```

```
              160                        165                        170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt     579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175             180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att     627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                    195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt     675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct     723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat     771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
            240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat     819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat     867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc     915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta     963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cat agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
            320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395
```

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tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400             405             410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415             420             425             430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
            435             440             445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450             455             460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465             470             475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480             485             490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca   1539
Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
495             500             505             510

acc atc aac gat ggg tct gtc ata tagatcggct gcgtktgcg             1582
Thr Ile Asn Asp Gly Ser Val Ile
            515
```

```
<210> 12
<211> 518
<212> PRT
<213> Zea mays

<400> 12

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile

 1               5                10               15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20              25              30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35              40                      45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50              55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65              70              75                      80
```

```
Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                 85              90                    95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
             100             105             110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
         115             120             125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
     130             135             140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145             150             155             160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
             165             170             175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
             180             185             190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
         195             200             205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
     210             215             220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225             230             235             240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
             245             250             255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
             260             265             270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
         275             280             285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
     290             295             300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305             310             315             320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
             325             330             335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
             340             345             350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
         355             360             365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
     370             375             380
```

```
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385             390             395             400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405             410             415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420             425             430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
            435             440             445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450             455             460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465             470             475             480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
            485             490             495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
            500             505             510

Asn Asp Gly Ser Val Ile

        515
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<210> 13
<211> 1582
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
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<222> (1578)
<223> k = g or t.

<400> 13
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95   100   105   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115   120   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130   135   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145   150   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160   165   170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175   180   185   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195   200   205

```
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
            240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
            320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att    1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
            400                 405                 410


gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg    1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430
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atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435             440             445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
                450             455             460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
                465             470             475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480             485             490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca   1539
Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
495             500             505             510

acc atc aac gat ggg tct gtc ata tagatcggct gcgtktgcg              1582
Thr Ile Asn Asp Gly Ser Val Ile
                515
```

<210> 14
<211> 518
<212> PRT
<213> Zea mays

<400> 14

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1               5               10              15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20              25              30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35              40              45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50              55              60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65              70              75              80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
            85              90              95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100             105             110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115             120             125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
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            130                      135                      140
```

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145   150   155   160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                        165   170   175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
                180   185   190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
                195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
                260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu

```
            435                   440                   445
    Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
        450                   455                   460
    Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
    465                   470                   475                   480
    Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
                          485                   490                   495
    Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
                500                   505                   510
    Asn Asp Gly Ser Val Ile
              515
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<210> 15
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 15
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac   51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta    99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15               20                  25                  30
```

```
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga    291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                 100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160                 165                 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                 245                 250
```

```
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat      819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat      867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                    275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc      915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta      963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt     1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
        320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc     1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag     1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                    355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc     1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc     1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att     1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg     1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta     1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata     1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg     1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475
```

```
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                     485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                     500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                    515
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<210> 16
<211> 516
<212> PRT
<213> Zea mays

<400> 16

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
             20              25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
         35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
     50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
             85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
```

```
              195                    200                    205

    Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210             215             220

    Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
    225             230             235             240

    Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                    245             250             255

    Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
                260             265             270

    Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275             280             285

    Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290             295             300

    Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
    305             310             315             320

    Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                325             330             335

    Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                340             345             350

    Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355             360             365

    Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
        370             375             380

    Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
    385             390             395             400

    Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405             410             415

    Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                420             425             430

    Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
                435             440             445

    Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
        450             455             460

    Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
    465             470             475             480

    Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485             490             495

    Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
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            500                    505                    510
Gly Ser Val Ile
          515


<210> 17
<211> 1576
<212> DNA
<213> Zea mays


<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable


<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.


<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.


<220>
<221> variation
<222> (1008)
<223> y = c or t.


<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.


<220>
<221> variation
<222> (1578)
<223> k = g or t.


<400> 17
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                    10


cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20                   25                   30


agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                   40                   45


ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
```

```
                 50                        55                        60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65                    70                    75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                    85                    90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95                      100                   105                   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                    115                   120                   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130                   135                   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                   150                   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160                   165                   170

gag cca ccn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                     180                   185                   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                    195                   200                   205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                   215                   220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                   230                   235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                   245                   250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                     260                   265                   270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
```

```
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
            275             280             285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290             295             300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305             310             315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
            320             325             330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335             340             345             350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355             360             365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370             375             380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385             390             395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
            400             405             410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415             420             425             430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435             440             445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450             455             460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465             470             475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480             485             490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
```

```
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495             500             505             510
```

```
aac gat ggg tct gtc ata tagatcggct gcgtktgcg                    1576
Asn Asp Gly Ser Val Ile
                515
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<210> 18
<211> 516
<212> PRT
<213> Zea mays

<400> 18

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1           5               10              15
```

```
Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20              25              30
```

```
Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35              40              45
```

```
Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50              55              60
```

```
Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65              70              75              80
```

```
Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85              90              95
```

```
Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100             105             110
```

```
Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115             120             125
```

```
Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130             135             140
```

```
Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145             150             155             160
```

```
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165             170             175
```

```
Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180             185             190
```

```
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
            195             200             205
```

```
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210             215             220
```

```
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
```

225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
            325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
            435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450   455   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465   470   475   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485   490   495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500   505   510

Gly Ser Val Ile
            515

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<210> 19
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1209)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1371)
<223> h = a or c or t/u.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 19
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1           5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15                 20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                50                  55                  60
```

```
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65                      70              75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga    291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                      85              90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95                      100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160             165             170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175             180             185             190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195             200             205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210             215             220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
        225             230             235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240             245             250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255             260             265             270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
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                        275                      280                      285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                      295                      300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
                305                      310                      315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
        320                      325                      330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                      340                      345                      350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                      360                      365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                      375                      380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385                      390                      395

tca cay ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att    1251
Ser His Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                      405                      410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg    1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                      420                      425                      430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta    1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                      440                      445

ctg tta gct ggg aag gtc ccr ath gga ata gga agg aac aca aag ata    1395
Leu Leu Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile
                450                      455                      460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg    1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
                465                      470                      475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                      485                      490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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495                 500             505             510
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aac gat ggg tct gtc ata tagatcggct gcgtktgcg                  1576
Asn Asp Gly Ser Val Ile
                    515
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<210> 20
<211> 516
<212> PRT
<213> Zea mays

<400> 20

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65              70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
            85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
            195                 200                 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210                 215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
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225                    230                    235                    240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245             250             255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260             265             270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275             280             285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290             295             300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305             310             315             320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
            325             330             335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340             345             350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355             360             365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370             375             380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser His
385             390             395             400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405             410             415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420             425             430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
        435             440             445

Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450             455             460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465             470             475             480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485             490             495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500             505             510

Gly Ser Val Ile
        515
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<210> 21
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (321)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 21
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                     35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                 50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
             65   70   75

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gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80              85              90

tct cag ctc ttt cct ctg aca agc aca acn gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro
95              100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
160             165             170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175             180             185             190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195             200             205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210             215             220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225             230             235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240             245             250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255             260             265             270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275             280             285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290             295             300
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aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305             310             315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
        320             325             330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335             340             345             350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
            355             360             365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370             375             380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385             390             395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att    1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400             405             410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg    1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415             420             425             430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta    1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
            435             440             445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata    1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450             455             460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg    1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465             470             475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480             485             490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495             500             505             510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
            515
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<210> 22
<211> 516
<212> PRT
<213> Zea mays

<400> 22
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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
           20              25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
       35              40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
   50              55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65              70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
           85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro Val Gly
           100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser

       115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
       130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
               165                 170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
           180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
           195                 200                 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
       210                 215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                 230                 235                 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
               245                 250                 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
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                  260                    265                    270

    Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275                    280                    285

    Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
            290                    295                    300

    Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
    305                    310                    315                    320

    Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
                    325                    330                    335

    Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                    340                    345                    350

    Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
                    355                    360                    365

    Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
            370                    375                    380

    Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
    385                    390                    395                    400

    Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                    405                    410                    415

    Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                    420                    425                    430

    Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
                    435                    440                    445

    Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
            450                    455                    460

    Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
    465                    470                    475                    480

    Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                    485                    490                    495

    Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
                    500                    505                    510

    Gly Ser Val Ile
            515


    <210> 23
    <211> 1576
    <212> DNA
    <213> Zea mays

    <220>
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<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1389)
<223> h = a or c or t/u.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 23
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                 35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
         65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
     80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

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                Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
                 95              100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc     387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
            115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act     435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac     483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa     531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
            160             165             170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt     579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175             180             185             190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att     627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195             200             205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt     675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210             215             220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct     723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225             230             235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat     771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
            240             245             250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat     819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255             260             265             270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat     867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
            275             280             285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc     915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290             295             300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta     963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305             310             315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt     1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
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              320                    325                      330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                    355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
            400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac ath aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile
                450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
            480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                515
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<210> 24
<211> 516
<212> PRT
<213> Zea mays

<400> 24
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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20              25              30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35              40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50              55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
            85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100             105             110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115             120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130             135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145             150             155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
            165             170             175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180             185             190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195             200             205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210             215             220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225             230             235             240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245             250             255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
        260             265             270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275             280             285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290             295             300
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Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
            325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile Arg Asn
    450   455   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465   470   475   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485   490   495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp

        500   505   510

Gly Ser Val Ile
        515

<210> 25
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>

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<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.


<220>
<221> variation
<222> (657)
<223> n = a or g or c or t/u, unknown, or other.


<220>
<221> variation
<222> (1008)
<223> y = c or t.


<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.


<220>
<221> variation
<222> (1578)
<223> k = g or t.


<400> 25
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac  51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta  99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20              25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt  147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35              40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct  195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50              55              60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat  243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65              70              75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga  291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80              85              90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct  339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95              100             105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc  387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
            115             120                 125
```

```
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
            160             165             170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175             180             185             190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195             200             205

gta atc ttg agt ggc gat cag ctt tat ccn atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu
            210             215             220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225             230             235


cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
            240             245             250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255             260             265             270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
            275             280             285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290             295             300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305             310             315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
            320             325             330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335             340             345             350
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aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
                450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
            480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg   1576
Asn Asp Gly Ser Val Ile
                515
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<210> 26
<211> 516
<212> PRT
<213> Zea mays

<400> 26

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
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              20                      25                      30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35              40              45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
        50              55              60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65              70              75              80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
            85              90              95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100             105             110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115             120             125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130             135             140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145             150             155             160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
            165             170             175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180             185             190


Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195             200             205

Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu Val Gln
    210             215             220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225             230             235             240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245             250             255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260             265             270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275             280             285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290             295             300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305             310             315             320
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```
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
            325             330             335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340             345             350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355             360             365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370             375             380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385             390             395             400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405             410             415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420             425             430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
            435             440             445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450             455             460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465             470             475             480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485             490             495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500             505             510

Gly Ser Val Ile
        515
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<210> 27
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
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<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1287)
<223> y = c or t.

<220>
<221> variation

<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 27
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
            80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95   100   105   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

```
                115                  120                    125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130              135                  140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145              150                  155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160              165                  170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175              180                  185                  190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                  200                  205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                  215                  220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                  230                  235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                  245                  250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                  260                  265                  270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat   867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                  280                  285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                  295                  300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                  310                  315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
        320                  325                  330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                  340                  345                  350
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aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
            355             360             365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370             375             380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385             390             395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400             405             410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa tty aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val
415             420             425             430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
            435             440             445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
        450             455             460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465             470             475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480             485             490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495             500             505             510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
            515
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<210> 28
<211> 516
<212> PRT
<213> Zea mays

<400> 28

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
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```
            20                      25                      30

    Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35              40              45

    Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
        50              55              60

    Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
    65              70              75              80

    Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85              90              95

    Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
                100             105             110

    Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115             120             125

    Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130             135             140

    Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
    145             150             155             160

    Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165             170             175

    Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
                180             185             190

    Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
                195             200             205

    Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210             215             220

    Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
    225             230             235             240

    Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245             250             255

    Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
                260             265             270

    Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275             280             285

    Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290             295             300

    Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
    305             310             315             320
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```
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
            325             330             335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340             345             350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
    355             360             365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370             375             380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385             390             395             400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405             410             415

Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met
            420             425             430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
            435             440             445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450             455             460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465             470             475             480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485             490             495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500             505             510

Gly Ser Val Ile
            515
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<210> 29
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
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<221> variation
<222> (981)
<223> r = g or a.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1086)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 29
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
         Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
           35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
       65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
    80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

95   100   105   110

```
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
            115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
            160                 165                 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
            240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
            275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315

cat gac ttt gga tct aar atc ctc cca aga gct gta cta gat cay agt    1011
His Asp Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser
            320                 325                 330
```

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gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc      1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335             340             345             350

aaa tca ttc ttt gat gca aac ttg gtn ctc act gag cag cct tcc aag      1107
Lys Ser Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys
                355             360             365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc      1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370             375             380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc      1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
        385             390             395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att      1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400             405             410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg      1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415             420             425             430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta      1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435             440             445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata      1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450             455             460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg      1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465             470             475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg      1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480             485             490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc      1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495             500             505             510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                         1576
Asn Asp Gly Ser Val Ile
                515
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<210> 30
<211> 516
<212> PRT
<213> Zea mays

<400> 30

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1   5   10   15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20   25   30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35   40   45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50   55   60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65   70   75   80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
            85   90   95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100   105   110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115   120   125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130   135   140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145   150   155   160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
            165   170   175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180   185   190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290   295   300

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Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305             310             315                         320

Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
            325             330                 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340             345                 350

Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355             360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370             375             380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385             390             395                         400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405             410                 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420             425                 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435             440                 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450             455                 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465             470             475                         480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485             490                 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500             505                 510

Gly Ser Val Ile
        515
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<210> 31
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
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<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 31
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
         Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
         1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
         35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
         50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
         65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
         80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95   100   105   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
         115   120   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
         130   135   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

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      Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
              145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa      531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160                 165                 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt      579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att      627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt      675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct      723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
                225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat      771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat      819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat      867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc      915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta      963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tty agt     1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser
        320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc     1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag     1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc     1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
```

                370   375   380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385   390   395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400   405   410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415   420   425   430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                    435   440   445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450   455   460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465   470   475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480   485   490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495   500   505   510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg   1576
Asn Asp Gly Ser Val Ile
                515

<210> 32
<211> 516
<212> PRT
<213> Zea mays

<400> 32

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1   5   10   15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20   25   30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35   40   45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50   55   60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65   70   75   80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85   90   95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100   105   110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115   120   125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130   135   140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145   150   155   160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165   170   175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180   185   190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser Val Gln
            325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
        420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
      435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
      450   455   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465   470   475   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
        485   490   495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
        500   505   510

Gly Ser Val Ile
      515

<210> 33
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
     heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

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<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 33
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac  51
          Met·Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1            5                   10


cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta  99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15              20                  25                  30


agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt  147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                  40                  45


ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct  195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50                  55                  60


tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat  243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65                  70                  75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga  291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
    80                  85                  90


tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct  339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95              100                 105                 110


gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc  387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                 120                 125


aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act  435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                 135                 140


tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac  483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145                 150                 155


ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa  531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                 165                 170


gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt  579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190


atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att  627
```

```
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195               200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210               215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225               230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
            240               245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255               260               265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
            275               280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290               295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305               310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser
            320               325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335               340               345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
            355               360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370               375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385               390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att    1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
            400               405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg    1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
```

```
         415                    420                    425                    430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta    1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                440                445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata    1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
                450                455                460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg    1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
                465                470                475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                485                490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                500                505                510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                515
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<210> 34
<211> 516
<212> PRT
<213> Zea mays

<400> 34

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1                5                  10                 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                 25                 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35                 40                 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                 55                 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                 70                 75                 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                 90                 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
                100                105                110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115                120                125
```

```
Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130             135             140
```

```
Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145             150             155             160
```

```
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
            165             170             175
```

```
Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180             185             190
```

```
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195             200             205
```

```
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210             215             220
```

```
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225             230             235             240
```

```
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245             250             255
```

```
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260             265             270
```

```
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275             280             285
```

```
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290             295             300
```

```
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305             310             315             320
```

```
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser Val Gln
            325             330             335
```

```
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340             345             350
```

```
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355             360             365
```

```
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370             375             380
```

```
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385             390             395             400
```

```
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405             410             415
```

```
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420             425             430
```

```
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435                 440             445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
        450                 455             460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470             475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485             490             495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500             505             510

Gly Ser Val Ile
        515
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<210> 35
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 35

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                    35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95   100   105   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115   120   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130   135   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145   150   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160   165   170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175   180   185   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195   200   205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210   215   220

```
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
        225             230             235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240             245             250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255             260             265             270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275             280             285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290             295             300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305             310             315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
        320             325             330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335             340             345             350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
            355             360             365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370             375             380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385             390             395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att    1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400             405             410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg    1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415             420             425             430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta    1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
            435             440             445
```

```
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450             455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465             470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480             485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
                515
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<210> 36
<211> 516
<212> PRT
<213> Zea mays

<400> 36

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
        50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160
```

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
              165   170   175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
              180   185   190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
          195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
              245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
              260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
          275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
              325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
          340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
          355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
              405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
              420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
          435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450   455   460

```
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465             470             475             480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485             490             495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500             505             510

Gly Ser Val Ile
        515
```

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<210> 37
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 37
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac   51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1               5                   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
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        15                    20                    25                    30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                    40                    45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                50                    55                    60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65                    70                    75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                    85                    90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95                    100                   105                   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                   120                   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130                   135                   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
                145                   150                   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160                   165                   170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                   180                   185                   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                   200                   205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                   215                   220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                   230                   235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
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    Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240             245             250

    cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
    His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
    255             260             265             270

    ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
    Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                    275             280             285

    gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
    Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290             295             300

    aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
    Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
                305             310             315

    cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
    His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
        320             325             330

    gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
    Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
    335             340             345             350

    aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
    Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                    355             360             365

    ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
    Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370             375             380

    ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc   1203
    Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
            385             390             395

    tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
    Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400             405             410

    gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
    Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
    415             420             425             430

    atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
    Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                    435             440             445

    ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
    Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
                450             455             460

    agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
    Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
```

```
                465                      470                          475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg     1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc     1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                        1576
Asn Asp Gly Ser Val Ile
                515
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<210> 38
<211> 516
<212> PRT
<213> Zea mays

<400> 38

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190
```

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
        260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
            325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
            435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450   455   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465   470   475   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485   490   495

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Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500                 505                 510

Gly Ser Val Ile
        515
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<210> 39
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 39
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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
            1           5                   10


cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20              25              30
```

```
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
                65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95                  100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                 165                 170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
                225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                 245                 250
```

```
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255             260             265             270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat   867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275             280             285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290             295             300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305             310             315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
            320             325             330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335             340             345             350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355             360             365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370             375             380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
            385             390             395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
            400             405             410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415             420             425             430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435             440             445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450             455             460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465             470             475
```

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atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480             485             490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495             500             505             510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
                515
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<210> 40
<211> 516
<212> PRT
<213> Zea mays

<400> 40

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
            195                 200                 205
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Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
            325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
        340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
            435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450   455   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465   470   475   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485   490   495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp

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          500                   505                   510
Gly Ser Val Ile
        515
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<210> 41
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 41
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
```

```
      Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                       35              40                  45

      ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
      Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                   50              55                  60

      tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
      Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
                   65              70                  75

      gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
      Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
                   80              85                  90

      tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
      Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
       95              100                 105                 110

      gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
      Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                       115                 120                 125

      aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
      Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                   130                 135                 140

      tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
      Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
                   145                 150                 155

      ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
      Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
           160                 165                 170

      gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
      Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
       175                 180                 185                 190

      atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
      Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                       195                 200                 205

      gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
      Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                       210                 215                 220

      gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
      Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
                   225                 230                 235

      cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
      Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
           240                 245                 250
```

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cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260             265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275             280             285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290             295             300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305             310             315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
        320             325             330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340             345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355             360             365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370             375             380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
            385             390             395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400             405             410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420             425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
            435             440             445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450             455             460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465             470             475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
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```
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                    515
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<210> 42
<211> 516
<212> PRT
<213> Zea mays

<400> 42

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
            195                 200                 205
```

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
        260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
    275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
            325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
        340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
    355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
        420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
    435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450   455   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465   470   475   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485   490   495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500   505   510

Gly Ser Val Ile
        515